

SEQUENCE LISTING

<110> Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.

<120> Immunokinases

<130> 042950wo Me/FM

<140> PCT/EP2005/050131

<141> 2005-01-13

<150> 04000847.6

<151> 2004-01-16

<150> 04017928.5

<151> 2004-07-29

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 1785

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

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<221> CDS

<222> (1)..(1785)

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<221> N_region

<222> (1)..(21)

<223> immunoglobulin kappa chain leader sequence

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ggt tcc act ggt gac tct aga atg gtc cag gcc tcg atg agg agc cca 96
Gly Ser Thr Gly Asp Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro
20 25 30

aat atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att 144
Asn Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile
35 40 45

gga gag gag ctg ggc agt ggc cag ttt gcc atc gtg aag aag tgc cgg 192
Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg
50 55 60

gag aag agc acg ggg ctg gag tat gca gcc aag ttc att aag aag agg 240
Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg
65 70 75 80

cag agc cgg gcc agc cgt cgg ggc gtg tgc cgg gag gaa atc gag cgg 288
Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg
85 90 95

gag gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg 336
Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu
100 105 110

cac gac gtc tat gag aac cgc acc gac gtg gtg ctc atc ctt gag cta 384

His	Asp	Val	Tyr	Glu	Asn	Arg	Thr	Asp	Val	Val	Leu	Ile	Leu	Glu	Leu		
115							120					125					
gtg	tcc	gga	gga	gaa	ctg	ttt	gat	ttc	ctg	gcc	cag	aag	gag	tcg	tta	432	
Val	Ser	Gly	Gly	Glu	Leu	Phe	Asp	Phe	Leu	Ala	Gln	Lys	Glu	Ser	Leu		
130					135					140							
agt	gag	gag	gaa	gcc	acc	agc	ttc	att	aag	cag	atc	ctg	gat	ggg	gtg	480	
Ser	Glu	Glu	Glu	Ala	Thr	Ser	Phe	Ile	Lys	Gln	Ile	Leu	Asp	Gly	Val		
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Asn	Tyr	Leu	His	Thr	Lys	Lys	Ile	Ala	His	Phe	Asp	Leu	Lys	Pro	Glu		
									165		170			175			
aac	atc	atg	ttg	tta	gac	aag	aat	atc	cca	att	cca	cac	atc	aag	ctg	576	
Asn	Ile	Met	Leu	Leu	Asp	Lys	Asn	Ile	Pro	Ile	Pro	His	Ile	Lys	Leu		
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Ile	Asp	Phe	Gly	Leu	Ala	His	Glu	Ile	Glu	Asp	Gly	Val	Glu	Phe	Lys		
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Asn	Ile	Phe	Gly	Thr	Pro	Glu	Phe	Val	Ala	Pro	Glu	Ile	Val	Asn	Tyr		
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Glu	Pro	Leu	Gly	Leu	Glu	Ala	Asp	Met	Trp	Ser	Ile	Gly	Val	Ile	Thr		
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Tyr	Ile	Leu	Leu	Ser	Gly	Ala	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln		
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gaa	acc	ctg	gca	aat	atc	act	gct	gtg	agt	tac	gac	ttt	gat	gag	gaa	816	
Glu	Thr	Leu	Ala	Asn	Ile	Thr	Ala	Val	Ser	Tyr	Asp	Phe	Asp	Glu	Glu		
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ttc	ttc	agc	cag	aca	agc	gag	ctg	gcc	aag	gac	ttc	att	cg	aag	ctt	864	
Phe	Phe	Ser	Gln	Thr	Ser	Glu	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Lys	Leu		
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ctt	gtg	aaa	gag	acc	cgg	aaa	cgg	ctt	acc	atc	caa	gag	gct	ctc	aga	912	
Leu	Val	Lys	Glu	Thr	Arg	Lys	Arg	Leu	Thr	Ile	Gln	Glu	Ala	Leu	Arg		
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cat	ccc	tgg	atc	gga	tcc	aaa	cta	gct	gag	cac	gaa	ggt	gac	gcg	gcc	960	
His	Pro	Trp	Ile	Gly	Ser	Lys	Leu	Ala	Glu	His	Glu	Gly	Asp	Ala	Ala		
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cag	ccg	gcc	atg	gcc	cag	gtc	aag	ctg	cag	gag	tca	ggg	act	gaa	ctg	1008	
Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Gln	Glu	Ser	Gly	Thr	Glu	Leu		
									325		330			335			
gca	aag	cct	ggg	gcc	gca	gtg	aag	atg	tcc	tgc	aag	gct	tct	ggc	tac	1056	
Ala	Lys	Pro	Gly	Ala	Ala	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr		
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acc	ttt	act	gac	tac	tgg	atg	cac	tgg	gtt	aaa	cag	agg	cct	gga	cag	1104	
Thr	Phe	Thr	Asp	Tyr	Trp	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln		
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Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	Pro	Asn	Thr	Ala	Tyr	Thr	Asp		
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Tyr	Asn	Gln	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser		

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Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser	Leu Thr Ser Glu Asp Ser			
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gca gtc tat tac tgt gca aaa aag aca act cag	act acg tgg ggg ttt			1296
Ala Val Tyr Tyr Cys Ala Lys Lys	Thr Thr Gln Thr Thr Trp Gly Phe			
420	425	430		
cct ttt tgg ggc caa ggg acc acg gtc acc	gtc tcc tca ggt gga ggc			1344
Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val	Ser Ser Gly Gly Gly			
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ggt tca ggc gga ggt ggc tct ggc ggt ggc	gga tcg gac att gtg ctg			1392
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser	Asp Ile Val Leu			
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acc cag tct cca aaa tcc atg gcc atg tca	gtc gga gag agg gtc acc			1440
Thr Gln Ser Pro Lys Ser Met Ala Met Ser	Val Gly Glu Arg Val			
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ttg agc tgc aag gcc agt gag aat gtg gat	tct ttt gtt tcc tgg tat			1488
Leu Ser Cys Lys Ala Ser Glu Asn Val Asp	Ser Phe Val Ser Trp Tyr			
485	490	495		
caa cag aaa cca ggc cag tct cct aaa	ctg ctg ata tac ggg gcc tcc			1536
Gln Gln Lys Pro Gly Gln Ser Pro Lys	Leu Ile Tyr Gly Ala Ser			
500	505	510		
aac cgg tac act ggg gtc ccc gat cgc ttc	gca ggc agt gga tct gga			1584
Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe	Ala Gly Ser Gly Ser Gly			
515	520	525		
aga gat ttc act ctg acc atc agc agt gtg	cag gct gaa gac ctt gca			1632
Arg Asp Phe Thr Leu Thr Ile Ser Ser Val	Gln Ala Glu Asp Leu Ala			
530	535	540		
gat tat cac tgt gga cag aat tac agg tat	ccg ctc acg ttc ggt gct			1680
Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr	Pro Leu Thr Phe Gly Ala			
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ggc acc aag ctg gaa atc aaa cgg gcg gcc	gca ggg ccc gaa caa aaa			1728
Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala	Gly Pro Glu Gln Lys			
565	570	575		
ctc atc tca gaa gag gat ctg aat agc	gcc gtc gac cat cat cat			1776
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His His				
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<210> 2

<211> 594

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:
pMS-(L-DAPK2'-Ki-4)-III/G open reading frame (ORF)

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Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro

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5

10

15

Gly Ser Thr Gly Asp Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro

20

25

30

Asn Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile

35

40

45

Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg
 50 55 60
 Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg
 65 70 75 80
 Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg
 85 90 95
 Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu
 100 105 110
 His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu
 115 120 125
 Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu
 130 135 140
 Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val
 145 150 155 160
 Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu
 165 170 175
 Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu
 180 185 190
 Ile Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys
 195 200 205
 Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr
 210 215 220
 Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr
 225 230 235 240
 Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln
 245 250 255
 Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu
 260 265 270
 Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu
 275 280 285
 Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg
 290 295 300
 His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala
 305 310 315 320
 Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr Glu Leu
 325 330 335
 Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser Gly Tyr
 340 345 350
 Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln
 355 360 365
 Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr Thr Asp
 370 375 380
 Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser
 385 390 395 400
 Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser
 405 410 415
 Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp Gly Phe
 420 425 430
 Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
 435 440 445
 Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Val Leu
 450 455 460
 Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg Val Thr
 465 470 475 480
 Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser Trp Tyr
 485 490 495
 Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser
 500 505 510
 Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly Ser Gly
 515 520 525
 Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala
 530 535 540
 Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe Gly Ala
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 Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
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 His His

<210> 3
<211> 1794

<212> DNA
<213> Artificial Sequence

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pMS-(K1-4-DAPK2')-II/G ORF

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<222> (1)..(1794)

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<222> (1)..(21)
<223> immunoglobulin kappa chain leader sequence
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 20 25 30

cag gag tca ggg act gaa ctg gca aag cct ggg gcc gca gtg aag atg	144		
Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met			
35	40	45	

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50				55					60							

gtt	aaa	cag	agg	cct	gga	cag	ggt	ctg	gaa	tgg	att	gga	tac	att	aat	240
Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Asn	
65				70					75						80	

cct aac act gct tat act gac tac aat cag aaa ttc aag gac aag gcc 288
 Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala
 85 90 95

aca ttg act gca gac aaa tcc tcc agc aca gcc tac atg caa ctg cgc 336
 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg
 100 105 110

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agc ctg acc tct gag gat tct gca gtc tat tac tgt gca aaa aag aca 384
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr
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act cag act acg tgg ggg ttt cct ttt tgg ggc caa ggg acc acg gtc 432
 Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val
 130 135 140

acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt 480
 Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 145 150 155 160

ggc gga tcg gac att gtg ctg acc cag tct cca aaa tcc atg gcc atg 528
 Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met
 165 170 175

tca gtc gga gag agg gtc acc ttg agc tgc aag gcc agt gag aat gtg 576
 Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val
 180 185 190

gat tct ttt gtt tcc tgg tat caa cag aaa cca ggc cag tct cct aaa	624
Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
195 200 205	
ctg ctg ata tac ggg gcc tcc aac cggt tac act ggg gtc ccc gat cgc	672
Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg	
210 215 220	
ttc gca ggc agt gga tct gga aga gat ttc act ctg acc atc agc agt	720
Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser	
225 230 235 240	
gtg cag gct gaa gac ctt gca gat tat cac tgt gga cag aat tac agg	768
Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg	
245 250 255	
tat ccg ctc acg ttc ggt gct ggc acc aag ctg gaa atc aaa cgg gcg	816
Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala	
260 265 270	
gcc gca ctc gag tct aga atg gtc cag gcc tcg atg agg agc cca aat	864
Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn	
275 280 285	
atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att gga	912
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290 295 300	
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Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu	
305 310 315 320	
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Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln	
325 330 335	
agc cgg gcc agc cgt cgg ggc gtg tgc cgg gag gaa atc gag cgg gag	1056
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Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu His	
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385 390 395 400	
gag gag gaa gcc acc agc ttc att aag cag atc ctg gat ggg gtg aat	1248
Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn	
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Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn	
420 425 430	
atc atg ttg tta gac aag aat atc cca att cca cac atc aag ctg att	1344
Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile	
435 440 445	
gac ttt ggc ctg gct cac gaa ata gaa gat gga gtt gaa ttt aaa aac	1392
Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn	
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gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac cat Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His 580 585 590	1776
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<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:
pMS-(Ki-4-DAPK2')-II/G ORF

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Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met
35 40 45
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp
50 55 60
Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
65 70 75 80
Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala
85 90 95
Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg
100 105 110
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr
115 120 125
Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val
130 135 140
Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
145 150 155 160
Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met
165 170 175
Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val
180 185 190

Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
 195 200 205
 Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
 210 215 220
 Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser
 225 230 235 240
 Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg
 245 250 255
 Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala
 260 265 270
 Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn
 275 280 285
 Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
 290 295 300
 Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu
 305 310 315 320
 Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln
 325 330 335
 Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg Glu
 340 345 350
 Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu His
 355 360 365
 Asp Leu Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu Val
 370 375 380
 Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser
 385 390 395 400
 Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn
 405 410 415
 Tyr Leu His Thr Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn
 420 425 430
 Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile
 435 440 445
 Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn
 450 455 460
 Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu
 465 470 475 480
 Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr
 485 490 495
 Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu
 500 505 510
 Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu Phe
 515 520 525
 Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu
 530 535 540
 Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His
 545 550 555 560
 Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Phe Arg Gly Gly Pro
 565 570 575
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His
 580 585 590
 His His His His
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: pMT-Ki-4
 (scFv)-eEF-2K ORF

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Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Leu Gly	
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Val Asp Gly Gly Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp	
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Lys His Met Pro Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala	
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Gly	Val	Arg	Gly	Met	Ala	Leu	Phe	Phe	Tyr	Ser	His	Ala	Cys	Asn	Arg	
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Gly	Asp	Glu	Asn	Met	Ser	Asp	Val	Thr	Phe	Asp	Ser	Leu	Pro	Ser	Ser	
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cca	gtc	ttc	agt	gac	ctc	gat	aac	atg	gca	tcc	aga	gac	cat	gat	cat	2208
Pro	Val	Phe	Ser	Asp	Leu	Asp	Asn	Met	Ala	Ser	Arg	Asp	His	Asp	His	
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gcc ctg cac tgg tac aac act gcc ctg gag atg acg gac tgt gat gag Ala Leu His Trp Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu 945 950 955 960			2880
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<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pMT-Ki-4
(scFv)-eEF-2K ORF

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 35 40 45
 Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr
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 Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser
 65 70 75 80
 Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro
 85 90 95
 Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr
 100 105 110
 Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp
 115 120 125
 Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu
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 Asp Ser Ala val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp
 145 150 155 160
 Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
 165 170 175
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile
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 Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met Ser val Gly Glu Arg
 195 200 205
 Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser
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 260 265 270
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 Ile Glu Pro Val Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln
 485 490 495
 Met Glu Ala Lys Leu Trp Gly Glu Glu Tyr Asn Arg His Lys Pro Pro
 500 505 510
 Lys Gln val Asp Ile Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg
 515 520 525
 Pro Gly Lys Pro Leu Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr
 530 535 540
 Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg
 545 550 555 560
 Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His

Gln Leu Ile Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp
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 Pro Gln Ile His Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu
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 Met Tyr Ser Gln Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic
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linker

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<220>
<223> Description of Artificial Sequence: c-Myc epitope

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domain IX of kinases

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